# Package: MOMA (via r-universe)

June 30, 2024

**Title** Multi Omic Master Regulator Analysis

**Version** 1.17.0

**Description** This package implements the inference of candidate master
regulator proteins from multi-omics' data (MOMA) algorithm, as
well as ancillary analysis and visualization functions.

**Depends** R (>= 4.0)

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**BugReports** https://github.com/califano-lab/MOMA/issues

**RoxygenNote** 7.1.0

**biocViews** Software, NetworkEnrichment, NetworkInference, Network,
FeatureExtraction, Clustering, FunctionalGenomics,
Transcriptomics, SystemsBiology

**Imports** circlize, cluster, ComplexHeatmap, dplyr, ggplot2, graphics,
grid, grDevices, magrittr, methods, MKmisc,
MultiAssayExperiment, parallel, qvalue, RColorBrewer, readr,
reshape2, rlang, stats, stringr, tibble, tidyr, utils

**Suggests** BiocStyle, knitr, rmarkdown, testthat, viper

**VignetteBuilder** knitr

**Repository** https://bioc.r-universe.dev

**RemoteUrl** https://github.com/bioc/MOMA

**RemoteRef** HEAD

**RemoteSha** f2d9ee40fb8cc9824e7321ac7711c6c7f270b8f4

# Contents

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cnvScoreStouffer                 *Integrate CNV scores*

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## Description

Integrate CNV scores

## Usage

```
cnvScoreStouffer(
  mapping,
  diggit.interactions,
  cytoband = TRUE,
  from.p = FALSE,
  pos.nes.only = TRUE
)
```

## Arguments

mapping              a named vector of genomic locations/cytoband IDs. names are the gene names
                     for each–i.e. a many to one mapping from HUGO or entrez IDs to cytoband
                     location

diggit.interactions

                     list indexed by MR/TF name in Entrez Space each points to a named vector of
                     NES / z-scores associated with entrez IDs for each interacting event.

cytoband             Boolean to use cytoband locations for computing final integrated score

from.p               Boolean, set TRUE if diggit.interaction values are p-values instead of z-scores

pos.nes.only         Boolean, only consider positive DIGGIT association scores when ranking can-
                     didate MRs (default=TRUE)

## Value

A vector of z-scores, named by the Master Regulators in 'diggit.interactions'

---

example.gbm.mae *Glioblastoma (GBM) Example Dataset*

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### Description

MultiAssayExperiment Object containing all the genomic assays needed to run the example code for MOMA

### Usage

```
example.gbm.mae
```

### Format

An MultiAssayExperiment object with 4 different sets of GBM assays

**viper** matrix of viper scores with samples in columns and regulators across the rows

**mut** matrix of samples and genes with potential mutations. 0 for no mutation, 1 for presence of some non-silent mutation

**cnv** matrix of samples and genes with copy number variant scores

---

gbm.pathways *Glioblastoma (GBM) Pathways*

---

### Description

Object containing information about the biological pathways that will be used in the analysis

### Usage

```
gbm.pathways
```

### Format

A list of lists named "cindy" and "preppi" respectively

**cindy** list of regulators, each with a set of modulators and p values representing their CINDY inferred association

**preppi** list of regulators, each with a set of potential binding partners and PREPPi inferred p values for probability of binding

---

gene.map                         *Gene Location Mapping*

---

### Description

Table used for converting between different forms of gene information. Downloaded from HGNC's custom download portal using the "Approved Symbol", "NCBI Gene ID", "Chromosome" and "Ensembl Gene ID" curated data options and only those with "Approved" status. Updated December 2019.

### Usage

```
gene.map
```

### Format

A Data frame with 4 columns

**Gene.Symbol**  Approved Symbol gene name

**Entrez.IDs**  NCBI Gene ID

**Cytoband**  Chromosome location

**Ensembl**  Ensembl gene ID

@source <https://www.genenames.org/download/custom/>

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makeSaturationPlots      *Main function to generate the summary plots of the analysis*

---

### Description

Main function to generate the summary plots of the analysis

### Usage

```
makeSaturationPlots(
  momaObj,
  clustering.solution = NULL,
  important.genes = NULL,
  fCNV = NULL,
  max.events = 30
)
```

## Arguments

momaObj           : momaObj that has already run the saturationCalculation function

clustering.solution

                  : clustering vector with sample names and cluster designations

important.genes

                  : vector of gene names to prioritize when plotting. Can be general genes of
                  interest, oncogenes, tumor supressors etc

fCNV              : vector of confirmed functional CNVs if calculated. Will filter for only those
                  CNVs

max.events        : maximum number of events to plot for the oncoplots

## Value

object with both types of summary plot for each subtype

## Examples

```
## Not run:
makeSaturationPlots(momaObj, max.events = 20)

## End(Not run)
```

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mapEntrez                *Convert from entrez ids to hugo gene names*

---

## Description

Convert from entrez ids to hugo gene names

## Usage

```
mapEntrez(entrez.ids)
```

## Arguments

entrez.ids        : vector of entrez ids requires hugo2entrez to be loaded

## Value

: vector of hugo gene names

## See Also

[mapHugo](mapHugo)

## Examples

```
mapEntrez(c("29974", "5728"))
```

---

mapHugo                       *Convert from hugo gene names to entrez ids*

---

### Description

Convert from hugo gene names to entrez ids

### Usage

```
mapHugo(hugo.ids)
```

### Arguments

hugo.ids            : vector of hugo gene names, requires hugo2entrez to be loaded

### Value

: vector of entrez ids

### See Also

[mapEntrez](#)

### Examples

```
mapHugo(c("A1CF","PTEN"))
```

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mapScoresCnvBand              *Map scores to cytoband location*

---

### Description

Map scores to cytoband location

### Usage

```
mapScoresCnvBand(
  mapping,
  diggit.interactions,
  from.p = FALSE,
  pos.nes.only = TRUE
)
```

**Arguments**

| | |
|---|---|
| mapping | a named vector of genomic locations/cytoband IDs. names are the gene names for each–i.e. a many to one mapping from HUGO or entrez IDs to cytoband location |
| diggit.interactions | |
| | list indexed by MR/TF name in Entrez Space |
| from.p | DIGGIT interactions are in p-value format instead of z-score (default=FALSE) |
| pos.nes.only | Only consider positive associations with NES scores (default=TRUE) each points to a named vector of NES / z-scores associated with entrez IDs for each interacting event. |

**Value**

A list of input scores, now named by cytoband location

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Moma-class                    *MOMA Object*

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**Description**

Main class encapsulating the input data and logic of the MOMA algorithm

**Fields**

viper matrix of inferred activity score inferred by viper

mut binary mutation matrix 1 for presence of mutation, 0 for not, NA if not determined

cnv matrix of cnv values. Can be binary or a range.

fusions binary matrix of fusion events if appliable

pathways list of pathways/connections to consider as extra evidence in the analysis

gene.blacklist character vector of genes to not include because of high mutation frequency

output.folder character vector of location to save files if desired

gene.loc.mapping data frame of gene names, entrez ids and cytoband locations

nes field for saving Normalized Enrichment Matrices from the associate events step

interactions field for saving the MR-interactions list

clustering.results results from clustering are saved here

ranks results field for ranking of MRs based on event association analysis

hypotheses results field for saving events that have enough occurences to be considered

genomic.saturation results field for genomic saturation analysis

coverage.summaryStats results field for genomic saturation analysis

checkpoints results field with the MRs determined to be the checkpoint for each cluster

sample.clustering field to save sample clustering vector. Numbers are cluster assignments, names are sample ids

## Methods

Cluster( clus.eval = c("reliability", "silhouette"), use.parallel = FALSE, cores = 1 )
  Cluster the samples after applying the MOMA weights to the VIPER scores

makeInteractions( genomic.event.types = c("amp", "del", "mut", "fus"), cindy.only = FALSE )
  Make interaction web for significant MRs based on their associated events

Rank( use.cindy = TRUE, genomic.event.types = c("amp", "del", "mut", "fus"), use.parallel = FALSE, cores =
  Rank MRs based on DIGGIT scores and number of associated events

runDIGGIT(fCNV = NULL, cnvthr = 0.5, min.events = 4, verbose = FALSE) Run DIGGIT asso-
  ciation function to get associations for driver genomic events

saturationCalculation( clustering.solution = NULL, cov.fraction = 0.85, topN = 100, verbose = FALSE )
  Calculate the number of MRs it takes to represent the desired coverage fraction of events

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MomaConstructor                    *MOMA Constructor Function*

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## Description

Create MOMA Object from either a MultiAssayExperiment object or a list of assays. See vignette
for more information on how to set up and run the MOMA object

## Usage

```
MomaConstructor(
  x,
  pathways,
  gene.blacklist = NA_character_,
  output.folder = NA_character_,
  gene.loc.mapping = gene.map,
  viperAssay = "viper",
  mutMat = "mut",
  cnvMat = "cnv",
  fusionMat = "fusion"
)
```

## Arguments

x                       A MultiAssayExerperiment object or list object with the following assays: (note:
                        by default assays must have these exact names. Otherwise they can be changed
                        using the viperAssay, mutMat, cnvMat and fusionMat parameters.)

                        **viper**  VIPER protein activity matrix with samples as columns and rows as pro-
                            tein IDs

                        **mut**  An indicator matrix (0/1) of mutation events with samples as columns and
                            genes as rows

                        **cnv**  A matrix of CNV scores (typically SNP6 array scores from TCGA) with
                            samples as columns and genes as rows

|  | **fusion** An indicator matrix (0/1) of fusion events with samples as columns and genes as rows |
|---|---|
| pathways | A named list of lists. Each named list represents interactions between proteins (keys) and their associated partners |
| gene.blacklist | A vector of genes to exclude from the analysis |
| output.folder | Location to store output and intermediate results |
| gene.loc.mapping | |
| | A data.frame of band locations and Entrez IDs |
| viperAssay | name associated with the viper assay in the assay object |
| mutMat | name associated with the mutation matrix in the assay object |
| cnvMat | name associated with the cnv matrix in the assay object |
| fusionMat | name associated with the fusion matrix in the assay object |

## Value

an instance of class Moma

## Examples

```
momaObj <- MomaConstructor(example.gbm.mae, gbm.pathways)
```

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| mutSig | *MutSig Blacklisted genes* |
|---|---|

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## Description

List of genes to not include in the DIGGIT mutation inference because they have been found to be mutated more often than expected by chance given background mutation processes.

## Usage

```
mutSig
```

## Format

A character vector of Entrez Gene IDs

## Source

<https://software.broadinstitute.org/cancer/cga/mutsig>

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| sampleNameFilter | *Retain TCGA sample ids without the final letter designation ('A/B/C')* |
|---|---|

---

### Description

Retain TCGA sample ids without the final letter designation ('A/B/C')

### Usage

```
sampleNameFilter(input, desired.len = 15)
```

### Arguments

| | |
|---|---|
| input | Matrix of expression or protein activity scores. Columns are sample names, rows are genes. Input can also just be an input vector of sample names. |
| desired.len | length to reduce strings to. Default is 15 because of TCGA naming conventions |

### Value

An identical matrix with new (shorter) column names, or a vector with the shortened names.

### Examples

```
sample.names <- c("TCGA-14-1825-01A", "TCGA-76-4931-01B", "TCGA-06-5418-01A")
sampleNameFilter(sample.names)
```

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| stoufferIntegrate | *dispatch method for either CNV location corrected or SNV* |
|---|---|

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### Description

dispatch method for either CNV location corrected or SNV

### Usage

```
stoufferIntegrate(interactions, cytoband.map = NULL)
```

### Arguments

| | |
|---|---|
| interactions | List of MR - Genomic Event interactions, inferred by DIGGIT |
| cytoband.map | Data.frame mapping Entrez.IDs to cytoband locations |

### Value

Z-scores for each MR

stoufferIntegrateDiggit

> *Use Stouffer's method to combine z-scores of DIGGIT interactions for each cMR protein.*

## Description

This function combines only positively associated DIGGIT scores by default to create a culmulative DIGGIT score for each cMR.

## Usage

```
stoufferIntegrateDiggit(interactions, from.p = FALSE, pos.nes.only = TRUE)
```

## Arguments

| | |
|---|---|
| interactions | A list indexed by TF, includes z-scores or p-values for each interacting event |
| from.p | Integrate p-values or z-scores (default z-scores; from.p = FALSE) |
| pos.nes.only | Use only positive NES scores to rank proteins (default TRUE) |

## Value

A list indexed by TF, a stouffer integrated z-score

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